

=> D HIS

(FILE 'HOME' ENTERED AT 13:18:35 ON 27 JAN 97)

INDEX 'AGRICOLA, AIDSLINE, ANABSTR, AQUASCI, BIOBUSINESS, BIOSIS,  
BIOTECHABS, BIOTECHDS, CABA, CANCERLIT, CAPLUS, CEABA, CEN, CIN,  
CJACS, CJELSEVIER, CONFSCI, CROPB, CROPU, DDFB, DDFU, DGENE,  
DISSABS, DRUGB, DRUGLAUNCH, DRUGNL, DRUGU, EMBAL, EMBASE, ...'  
ENTERED AT 13:22:35 ON 27 JAN 97

SEA ((TUMOUR? OR TUMOR?) (W) NECROSIS FACTOR) (3A) RECEPTOR?

-----  
8 FILE AGRICOLA  
110 FILE AIDSLINE  
2 FILE ANABSTR  
15 FILE BIOBUSINESS  
1915 FILE BIOSIS  
83 FILE BIOTECHABS  
83 FILE BIOTECHDS  
41 FILE CABA  
1623 FILE CANCERLIT  
1717 FILE CAPLUS  
18 FILE CEABA  
1 FILE CEN  
12 FILE CIN  
15 FILE CJACS  
58 FILE CONFSCI  
94 FILE DDFU  
249 FILE DGENE  
15 FILE DISSABS  
7 FILE DRUGNL  
100 FILE DRUGU  
40 FILE EMBAL  
1308 FILE EMBASE  
1 FILE FSTA  
318 FILE GENBANK  
16 FILE IFIPAT  
30 FILE JICST-EPLUS  
466 FILE LIFESCI  
1564 FILE MEDLINE  
3 FILE NTIS  
1 FILE PHIC  
15 FILE PHIN  
57 FILE PROMT  
1098 FILE SCISEARCH  
368 FILE TOXLINE  
131 FILE TOXLIT  
47 FILE USPATFULL

L1 QUE ((TUMOUR? OR TUMOR?) (W) NECROSIS FACTOR) (3A) RECEPTOR

-----  
SEA L1 AND (CLON? OR CDNA OR DNA OR RNA OR MRNA)

-----  
5 FILE AGRICOLA  
34 FILE AIDSLINE

2 FILE BIOBUSINESS  
 401 FILE BIOSIS  
 66 FILE BIOTECHABS  
 66 FILE BIOTECHDS  
 18 FILE CABA  
 502 FILE CANCERLIT  
 519 FILE CAPLUS  
 8 FILE CEABA  
 4 FILE CIN  
 11 FILE CJACS  
 1 FILE CONFSCI  
 16 FILE DDFU  
 137 FILE DGENE  
 5 FILE DISSABS  
 1 FILE DRUGNL  
 20 FILE DRUGU  
 8 FILE EMBAL  
 359 FILE EMBASE  
 1 FILE FSTA  
 318 FILE GENBANK  
 7 FILE IFIPAT  
 9 FILE JICST-EPLUS  
 137 FILE LIFESCI  
 489 FILE MEDLINE  
 3 FILE NTIS  
 1 FILE PHIN  
 12 FILE PROMT  
 417 FILE SCISEARCH  
 106 FILE TOXLINE  
 54 FILE TOXLIT  
 44 FILE USPATFULL  
 L2 QUE L1 AND (CLON? OR CDNA OR DNA OR RNA OR MRNA)

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FILE 'BIOSIS, CAPLUS, CANCERLIT, EMBASE, MEDLINE, SCISEARCH'  
 ENTERED AT 13:32:42 ON 27 JAN 97  
 L3 401 FILE BIOSIS  
 L4 519 FILE CAPLUS  
 L5 502 FILE CANCERLIT  
 L6 359 FILE EMBASE  
 L7 489 FILE MEDLINE  
 L8 417 FILE SCISEARCH  
 TOTAL FOR ALL FILES  
 L9 2687 S L2  
 L10 1095 DUP REM L9 (1592 DUPLICATES REMOVED)  
 E GREENE J/AU  
 L11 141 FILE BIOSIS  
 L12 87 FILE CAPLUS  
 L13 16 FILE CANCERLIT  
 L14 71 FILE EMBASE  
 L15 115 FILE MEDLINE  
 L16 268 FILE SCISEARCH  
 TOTAL FOR ALL FILES  
 L17 698 S E3 OR E26 OR E75 OR E78-79  
 L18 0 FILE BIOSIS  
 L19 1 FILE CAPLUS  
 L20 0 FILE CANCERLIT  
 L21 0 FILE EMBASE

L22 0 FILE MEDLINE  
L23 0 FILE SCISEARCH  
TOTAL FOR ALL FILES  
L24 1 S L17 AND L2  
E FLEISCHMANN R/AU  
L25 74 FILE BIOSIS  
L26 103 FILE CAPLUS  
L27 16 FILE CANCERLIT  
L28 49 FILE EMBASE  
L29 49 FILE MEDLINE  
L30 92 FILE SCISEARCH

TOTAL FOR ALL FILES

L31 383 S E3 OR E6 OR E13-15  
L32 0 FILE BIOSIS  
L33 1 FILE CAPLUS  
L34 0 FILE CANCERLIT  
L35 0 FILE EMBASE  
L36 0 FILE MEDLINE  
L37 0 FILE SCISEARCH

TOTAL FOR ALL FILES

L38 1 S L31 AND L2

FILE 'WPIDS' ENTERED AT 13:56:09 ON 27 JAN 97

L39 18 S L2  
E GREENE J/AU  
L40 0 S E3 AND E11  
L41 31 S E3 OR E11  
L42 0 S L41 AND L2

Doc. Ref. AS8  
Appl. No. 08/469,637

```

RESULT 13
LOCUS HSC0BE062 253 bp RNA EST 26-OCT-1994
DEFINITION H. sapiens partial cDNA sequence; clone c-0be06.
ACCESSION Z38433
NID g560441
KEYWORDS partial cDNA sequence; transcribed sequence fragment.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 253)
AUTHORS Genexpress.
TITLE Direct Submission
JOURNAL Submitted (24-OCT-1994) to the EMBL/GenBank/DBJ databases.
Genethon, B.P. 60, 91002 Evry Cedex France and Genetique
Moleculaire et Biologie du developpement, CNRS UPR420 B.P. 8, 94801
Villejuif Cedex France.E-mail: genexpress@genethon.fr
REFERENCE 2 (bases 1 to 253)
AUTHORS Genexpress.

TITLE The Genexpress cDNA program
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 253)
AUTHORS Auffray,C., Behar,G., Bois,F., Boucher,C., da Silva,C.,
Devignes,M.D., Duprat,S., Houlgatte,R., Jumeau,M.N., Lamy,B.,
Lorenzo,F., Mitchell,H., Mariage-Samson,R., Pietu,G., Pouliot,Y.,
Sebastiani-Kabaktchis,C. and Tessier,A.
TITLE IMAGE: Integrated molecular analysis of the human genome and its
expression
JOURNAL C.R. Acad. Sci., III, Sci. Vie 318, 263-272 (1995)
COMMENT Clone library from B.Souares, Psychiatry Dept. Columbia University
USA;

Cloning_method: total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA
vector;
Sequencing_method: single read, full automatic;
Primer: (-21)M13_universal;
cDNA sequence complementary to mRNA (3'end)
Stretch_removed: 31 T removed at sequence 5'end
Normalization_method: Bento Soares, P.N.A.S in press;
Genexpress_library_idt: C;
Genexpress_sequence_idt: alc-0be06;

No significant homology found with :
genbank release 81 swissprot release 28.

NCBI gi: 560441
FEATURES
source Location/Qualifiers
1..253
/organism="Homo sapiens"
/dev_stage="3 months old"
/isolate="muscular atrophy patient"
/tissue_type="total brain"
/clone_lib="normalized infant brain cDNA"
/sex="Female"

BASE COUNT 76 a 57 c 49 g 70 t 1 others
ORIGIN

Query Match 1.4%; Score 21; DB 34; Length 253;
Best Local Similarity 78.4%; Pred. No. 1.07e-02;
Matches 29; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 123 acacagctcacatgtacagacaataaaactgctcaag 159
|||||
QY 774 ACACAGCTCACAAGAACAGACTTCCAGCTGCTGAAG 810

```

RESULT 2  
LOCUS CRAGF1 1933 bp mRNA VRT 01-SEP-1993  
DEFINITION Carassius auratus (GFAP-1) mRNA, complete cds.  
ACCESSION L23876  
NID g388622  
KEYWORDS  
SOURCE Carassius auratus adult retina cDNA to mRNA.  
ORGANISM Carassius auratus  
Eukaryota; Animalia; Chordata; Vertebrata; Osteichthyes;  
Actinopterygii; Cypriniformes; Cyprinidae; Cyprinidae.  
REFERENCE 1 (bases 1 to 1933)  
AUTHORS Glasgow, E. and Schechter, N.  
TITLE Nucleotide sequence of a GFAP - like intermediate filament cDNA  
from Goldfish retina  
JOURNAL Unpublished (1993)  
COMMENT NCBI gi: 388622  
FEATURES  
source Location/Qualifiers  
1..1933  
/organism="Carassius auratus"  
/dev\_stage="adult"  
/sequenced\_mol="cDNA to mRNA"  
/tissue\_type="retina"  
CDS  
20..1099  
/gene="GFAP-1"  
/note="putative; NCBI gi: 388623"  
/codon\_start=1  
/db\_xref="PID:g388623"  
/translation="MGLNDRFASYIEKVRFLQNKMLVAELNQLRGKEPSRLGDIYQ  
EELRELRRQVDGLNAGKARLEIERDNLASDLATLKQRLQEEALRQEAENNLNFRQD  
VDEAALNRVQLERKIDALQDEISFLRKVHEEMRQLQEQVHVLDLVDVSKPDLTT  
ALKEIRAQFEAMATSNMQETEEWYRSKFADLTDAAGRNAELRQAEANEYRRQIQG  
LTCDLSELRGSNESLERQLREMEERFAIETAGYQDTVARLEDEIQMLKEEMARHLQY  
QDLLNVKLALDIEIATYRKLEGEESRITVPVQNFNTLQFRDTSLDTKLTPEAHVKRS  
IVVRTVETRDGEIIEKSTTERKDLP"  
BASE COUNT 561 a 395 c 507 g 470 t  
ORIGIN  
Query Match 1.6%; Score 25; DB 77; Length 1933;  
Best Local Similarity 77.8%; Pred. No. 1.22e-01;  
Matches 35; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
Db 901 gaagctgctcgaaggagaggaaagcagaatcactgttccggtgca 945  
|||||  
Cp 931 GAAGCTGCTCGAAGGTGAGGTTAGCATGTCCAATGTGCCGCTGCA 887

Doc. Ref. **AR9**  
Appl. No. 08/469,637

**RESULT** 7  
**LOCUS** H14106 344 bp mRNA EST 10-JUL-1995  
**DEFINITION** ym62a05.r1 Homo sapiens cDNA clone 163472 5' similar to SP:S32367  
S32367 ALPA-SNAP PROTEIN  
**ACCESSION** H14106  
**NID** g878954  
**KEYWORDS** EST.  
**SOURCE** human clone-163472 library-Soares adult brain N2b4HB55Y vector-pT7T3D (Pharmacia) with a modified polylinker host-DH10B (ampicillin resistant) primer-M13RP1 Rsite1-Not I Rsite2-Eco RI 55-year old male. 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCGCTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 53. Library constructed by Bento Soares and M.Fatima Bonaldo. The adult brain RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 hours after death which occurred in consequence of a ruptured aortic aneurysm. RNA was prepared from a pool of tissues representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, subcortical white matter, basal ganglia, thalamus, cerebellum, midbrain, pons and medulla.

**ORGANISM** Homo sapiens  
Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

**REFERENCE** 1 (bases 1 to 344)  
**AUTHORS** Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevasakis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.  
**TITLE** The WashU-Merck EST Project  
**JOURNAL** Unpublished (1995)

**COMMENT**  
Contact: Wilson RK  
WashU-Merck EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
High quality sequence stops: 313  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

**FEATURES**  
**source** NCBI gi: 878954  
Location/Qualifiers  
1..344  
/organism="Homo sapiens"  
/clone="163472"  
/note="human"

**BASE COUNT** 71 a 116 c 86 g 64 t 7 others  
**ORIGIN**

Query Match 1.5%; Score 23; DB 8; Length 344;  
Best Local Similarity 77.8%; Pred. No. 2.98e-05;  
Matches 28; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Db 117 gcaccacttcccctnactactnctacncacacagct 152  
|| ||| ||| ||| ||| ||| ||| |||  
Qy 230 GCGCCCCCTGCCCCTGACCCTACTACACAGACAGCT 265

RESULT 12  
LOCUS G11923 245 bp DNA STS 23-OCT-1995  
DEFINITION human STS MR4116.  
ACCESSION G11923  
NID gl036742  
KEYWORDS STS sequence; primer; sequence tagged site.  
SOURCE human STSs derived from random genomic DNA.  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 245)  
AUTHORS Hudson, T.  
TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
Mapped STSs  
JOURNAL Unpublished (1995)  
COMMENT  
Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: TGTTTGTAGTTGTTTGTATTGGA  
Primer B: AAAGGAGTCAAATGGGTTTTT

STS size: 100

PCR Profile:

Presoak:

Denaturation:

Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pM

dNTPs: each 4 nM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCL: 10 mM

pH: 9.3

Prepared with primer pairs derived from random genomic sequence.

NCBI gi: 1036742  
FEATURES  
source Location/Qualifiers  
1..245  
/organism="Homo sapiens"  
/note="human"  
STS 56..155  
/map="791\_B\_4; 816\_F\_6; 921\_C\_9; 928\_A\_7; 934\_F\_6;  
963\_G\_6"  
primer\_bind 56..80  
/map="791\_B\_4; 816\_F\_6; 921\_C\_9; 928\_A\_7; 934\_F\_6;  
963\_G\_6"  
primer\_bind complement(134..155)  
/map="791\_B\_4; 816\_F\_6; 921\_C\_9; 928\_A\_7; 934\_F\_6;  
963\_G\_6"  
BASE COUNT 92 a 28 c 35 g 87 t 3 others  
ORIGIN

Query Match 1.4%; Score 21; DB 95; Length 245;

Best Local Similarity 70.8%; Pred. No. 1.07e-02;

Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Db 109 tnccttgaaatgttacctcatttaaaaaaacccattttgactcctttt 156  
| ||| | ||| | ||||| | || ||||| | ||| |||||  
Cp 519 TGCTTTAGATGACGTCTCATTGAGAAGAACCCTCTGGACATCTTTT 472

RESULT 3  
LOCUS RRMAP1B5 7095 bp RNA ROD 21-OCT-1992  
DEFINITION R.norvegicus mRNA for microtubule associated protein IB.  
ACCESSION X60370 X60371 X60550  
NID g57618

KEYWORDS MAP1B gene; microtubule-associated protein.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Glires; Rodentia;  
Sciurognathi; Myomorpha; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 7095)  
AUTHORS Zauner, W., Kratz, J., Staunton, J., Feick, P. and Wiche, G.  
TITLE Identification of two distinct microtubule binding domains on  
recombinant rat MAP 1B  
JOURNAL Eur. J. Cell Biol. 57 (1), 66-74 (1992)  
MEDLINE 92347374

REFERENCE 2 (bases 1 to 7095)  
AUTHORS Wiche, G.  
TITLE Direct Submission  
JOURNAL Submitted (07-AUG-1991) to the EMBL/GenBank/DDBJ databases. G.  
Wiche, Inst of Biochemistry, University of Vienna,  
Wahringerstrasse 17, 1090 Vienna, AUSTRIA

REMARK revised by [3]  
REFERENCE 3 (bases 1 to 7095)  
AUTHORS Wiche, G.  
TITLE Direct Submission  
JOURNAL Submitted (07-AUG-1992) to the EMBL/GenBank/DDBJ databases. G.  
Wiche, Institute of Biochemistry and Molecular Biology, University  
of Vienna, Dr. Bohrgasse 9, 1030 Vienna, AUSTRIA

COMMENT NCBI gi: 57618  
FEATURES  
source Location/Qualifiers  
1..7095  
/organism="Rattus norvegicus"  
/strain="Sprague-Dawley"  
/dev\_stage="adult"  
/tissue\_type="brain"  
/cell\_type="C6 glioma"

BASE COUNT 2124 a 1856 c 1799 g 1316 t  
ORIGIN

Query Match 1.6%; Score 24; DB 66; Length 7095;  
Best Local Similarity 76.1%; Pred. No. 5.70e-01;  
Matches 35; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Db 1004 gcaaggaaatgcagttatttcagtcagcagtggaaccaacaa 1049  
||||| ||||| ||| ||||| ||||| ||||| ||||| |||||  
Qy 305 GCAAGGAGCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAA 350



Appl. No. 08/469,637

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RESULT 11
ID R38859 standard; Protein; 277 AA.
AC R38859;
DT 07-FEB-1994 (first entry)
DE CD40 protein.
KW Receptor; ligand; B-cell; T-cell; allergy; autoimmunity; antibody.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Domain 194..277
FT /label= Transmembrane domain.
PN EP-555880-A.
PD 18-AUG-1993.
PF 12-FEB-1993; 102279.
PR 14-FEB-1992; US-835799.
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
PA (DART-) DARTMOUTH COLLEGE.
PA (GEO ) GEN HOSPITAL CORP.
PI Aruffo AA, Ledbetter JA, Noell R, Stamenkovic I,
PI Noelle R;
DR WPI; 93-260142/33.
DR N-PSDB; Q47341.
PT CD40CR receptor and its' ligands - used to inhibit B-cell
PT activation in allergy and auto-immune disease
PS Claim 1; Figure 8a; 21pp; English.
CC The CD40CR receptor is a counter receptor for the CD40 B-cell
CC antigen. It is also a receptor for ligands (sometimes fusion
CC molecules) comprising part of the CD40 protein. A soluble
CC CD40/immunoglobulin fusion protein is able to inhibit helper T-cell
CC mediated B-cell activation by binding to the CD40 receptor on
CC T-cell membranes. Purified receptor provides a means of
CC controlling B-cell activation which may be useful in the treatment
CC of allergy and autoimmune disease.
SQ Sequence 277 AA;

Query Match 9.9%; Score 301; DB 7; Length 277;
Best Local Similarity 36.8%; Pred. No. 5.78e-18;
Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;

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Db      38 cs|lcqpggk|lv|sdcteftetec|lpccesefl|dtwnr|ethchqhkycdpn-lglr-vqqkg 95
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Qy     41 CDKCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDEC-L-YCSPVCKELQYVKQECC 97
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db     96 tsetdtictceegwhctseacescvlhrcspgfgvkqiatgvsd|ticepcpv|gffsnvs 155
        :   :   |   ||:   |   |   |   ||||:||||   |   |   |   |   |   |
Qy    98 NRTHNRVCECKEGRY-L-EI-EFCLKHRSCPPGFGVVQAGTPERNTVCKRCPDGFFSNET 154
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db    156 safekchpwts|cetkd|lvvqqagtnkt|dvvcg 187
        |:   |:   |:   |:   |:   |:   |:   |:   |:   |:   |:   |:   |:
Qy    155 SSKAPCRKHNTNCSVFGLLLTQKGNATHDNICS 186

```

RESULT 7  
LOCUS HSLIPA4 1851 bp DNA  
DEFINITION H.sapiens LIPA gene, exon 4. PRI 01-MAR-1994  
ACCESSION X75491  
NID g443925  
KEYWORDS acid cholesteryl ester hydrolase; lipA gene;  
lysosomal acid lipase.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group;  
Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata;  
Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata;  
Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates;  
Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1851)  
AUTHORS Aslanidis, C., Klima, H., Lackner, K.J. and Schmitz, G.  
TITLE Genomic organization of the human lysosomal acid lipase gene (LIPA)  
JOURNAL Genomics 20 (2), 329-331 (1994)  
MEDLINE 94292225  
REFERENCE 2 (bases 1 to 1851)  
AUTHORS Aslanidis, C.  
TITLE Direct Submission  
JOURNAL Submitted (02-NOV-1993) to the EMBL/GenBank/DBJ databases. C.  
Aslanidis, Inst for Clinical Chemistry & Lab. Med., University of  
Regensburg, 93042 Regensburg, FRG  
COMMENT NCBI gi: 443925  
FEATURES  
source Location/Qualifiers  
1..1851  
/organism="Homo sapiens"  
/clone\_lib="human placenta DNA cloned in lambda FIXII  
(stratagene)"  
/chromosome="10q23.2-q23.3"  
intron <1..948  
/number=3  
CDS 949..1137  
/gene="LIPA"  
/EC\_number="3.1.1.13"  
/product="sterol esterase"  
exon 949..1137  
/gene="LIPA"  
/number=4  
/usedin=x75489:LIPA\_CDS  
/usedin=x75489:LIPA\_mRNA  
intron 1138..>1851  
/number=4  
BASE COUNT 481 a 347 c 369 g 653 t 1 others  
ORIGIN  
Query Match 1.5%; Score 23; DB 51; Length 1851;  
Best Local Similarity 78.0%; Pred. No. 2.52e+00;  
Matches 32; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Db 662 ttcttaaaaaatatattgatttttgttttgctgcttacataa 702  
||||| ||||| ||| ||||| ||||| ||||| |||||  
Cp 851 TTCTTGACTATATCTTGGTCTTGTGTTTGATGTTCCATAA 811